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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/934,706

DATE: 11/16/2001

TIME: 08:59:09

Input Set : A:\substitute SL 029650-103.txt

Output Set: N:\CRF3\11162001\I934706.raw

ENTERED

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3 <110> APPLICANT: Terumo Corporation
W--> 4 <120> TITLE OF INVENTION: Functional Hybrid Polypeptide with Collagen-binding
W--> 5 Activity
W--> 6 <130> FILE REFERENCE: 19990120
W--> 7 <140> CURRENT APPLICATION NUMBER: WO, PCT/JP00/00964
C--> 8 <141> CURRENT FILING DATE: 2001-08-23
W--> 9 <160> NUMBER OF SEQ ID: 16
10 <170> SOFTWARE:
W--> 11 <210> SEQ ID NO: 1
12 <211> LENGTH: 343
13 <212> TYPE: PRT
14 <213> ORGANISM: Artificial Sequence
W--> 15 <220> FEATURE:
16 <223> OTHER INFORMATION: Description of Artificial Sequence:Modified Human
17 Fibronectin Collagen-Binding Domain
W--> 18 <220> FEATURE:
W--> 19 <221> NAME/KEY: INIT _MET
20 <222> LOCATION: (1)
W--> 21 <220> FEATURE:
22 <221> NAME/KEY: DOMAIN
23 <222> LOCATION: (2)..(341)
24 <223> OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
W--> 25 <220> FEATURE:
26 <221> NAME/KEY: CONFLICT
27 <222> LOCATION: (69).
W--> 28 <220> FEATURE:
29 <221> NAME/KEY: CONFLICT
30 <222> LOCATION: (125)
W--> 31 <400> SEQUENCE: 1
32 Met Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Tyr
33 1 5 10 15
34 Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met Gln
35 20 25 30
36 Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu Gly
37 35 40 45
38 Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly Gly
39 50 55 60
40 Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly Arg
41 65 70 75 80
42 Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu Trp
43 85 90 95
44 Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser Phe Cys
45 100 105 110
46 Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn Gly
47 115 120 125
48 Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr Thr Asp
49 130 135 140

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```

50  Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly Thr Thr
51  145                      150                      155                      160
52  Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met Ala Ala
53                      165                      170                      175
54  His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg Ile Gly
55                      180                      185                      190
56  Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg Cys Thr
57                      195                      200                      205
58  Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser Gln
59                      210                      215                      220
60  Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn Asp
61  225                      230                      235                      240
62  Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr Cys
63                      245                      250                      255
64  Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln Cys
65                      260                      265                      270
66  Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp Glu
67                      275                      280                      285
68  Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg Gly
69                      290                      295                      300
70  Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser Ser
71  305                      310                      315                      320
72  Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn Ser
73                      325                      330                      335
74  His Pro Ile Gln Trp Leu Glu
75                      340
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 159
78 <212> TYPE: PRT
79 <213> ORGANISM: Artificial Sequence
W--> 80 <220> FEATURE:
81 <223> OTHER INFORMATION: Description of Artificial Sequence:Human Basic
82      Fibroblast Growth Factor with Enterokinase
83      Recognition Sequence
W--> 84 <220> FEATURE:
85 <221> NAME/KEY: PEPTIDE
86 <222> LOCATION: (1)..(5)
87 <223> OTHER INFORMATION: /note="enterokinase recognition sequence"
W--> 88 <220> FEATURE:
89 <221> NAME/KEY: PEPTIDE
90 <222> LOCATION: (6)..(159)
91 <223> OTHER INFORMATION: /note="human fibroblast growth factor"
W--> 92 <400> SEQUENCE: 2
93  Asp Asp Asp Asp Lys Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu
94  1                      5                      10                      15
95  Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp
96                      20                      25                      30
97  Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His
98                      35                      40                      45

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```

99  Pro Asp Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile
100      50                      55                      60
101  Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly
102      65                      70                      75                      80
103  Val Cys Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu
104                      85                      90                      95
105  Ala Ser Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu
106      100                      105                      110
107  Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr
108      115                      120                      125
109  Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly
110      130                      135                      140
111  Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
112      145                      150                      155
113 <210> SEQ ID NO: 3
114 <211> LENGTH: 58
115 <212> TYPE: PRT
116 <213> ORGANISM: Artificial Sequence
W--> 117 <220> FEATURE:
118 <223> OTHER INFORMATION: Description of Artificial Sequence:Human Epidermal
119      Growth Factor with Enterokinase Recognition
120      Sequence
W--> 121 <220> FEATURE:
122 <221> NAME/KEY: PEPTIDE
123 <222> LOCATION: (1)..(5)
124 <223> OTHER INFORMATION: /note="enterokinase recognition sequence"
W--> 125 <220> FEATURE:
126 <221> NAME/KEY: PEPTIDE
127 <222> LOCATION: (6)..(58)
128 <223> OTHER INFORMATION: /note="human epidermal growth factor"
W--> 129 <400> SEQUENCE: 3
130  Asp Asp Asp Asp Lys Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp
131      1                      5                      10                      15
132  Gly Tyr Cys Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp
133      20                      25                      30
134  Lys Tyr Ala Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln
135      35                      40                      45
136  Tyr Arg Asp Leu Lys Trp Trp Glu Leu Arg
137      50                      55
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 501
140 <212> TYPE: PRT
141 <213> ORGANISM: Artificial Sequence
W--> 142 <220> FEATURE:
143 <223> OTHER INFORMATION: Description of Artificial Sequence:Hybrid
144      Polypeptide of Human Fibronectin Collagen-Binding
145      Domain and Human Basic Fibroblast Growth Factor
W--> 146 <220> FEATURE:
W--> 147 <221> NAME/KEY: INIT _MET

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148 <222> LOCATION: (1)
W--> 149 <220> FEATURE:
150 <221> NAME/KEY: DOMAIN
151 <222> LOCATION: (2)..(341)
152 <223> OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
W--> 153 <220> FEATURE:
154 <221> NAME/KEY: PEPTIDE
155 <222> LOCATION: (343)..(347)
156 <223> OTHER INFORMATION: /note="enterokinase recognition sequence"
W--> 157 <220> FEATURE:
158 <221> NAME/KEY: PEPTIDE
159 <222> LOCATION: (348)..(501)
160 <223> OTHER INFORMATION: /note="human fibroblast growth factor"
W--> 161 <400> SEQUENCE: 4
162 Met Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro Pro Pro Tyr
163   1           5           10           15
164 Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val Gly Met Gln
165           20           25           30
166 Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr Cys Leu Gly
167           35           40           45
168 Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr Tyr Gly Gly
169           50           55           60
170 Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly Arg
171           65           70           75           80
172 Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu Trp
173           85           90           95
174 Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr Ser Phe Cys
175           100          105          110
176 Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn Gly
177           115          120          125
178 Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn Tyr Thr Asp
179           130          135          140
180 Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys Gly Thr Thr
181           145          150          155          160
182 Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro Met Ala Ala
183           165          170          175
184 His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr Arg Ile Gly
185           180          185          190
186 Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met Arg Cys Thr
187           195          200          205
188 Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser Gln
189           210          215          220
190 Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn Val Asn Asp
191           225          230          235          240
192 Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn Cys Thr Cys
193           245          250          255
194 Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val Asp Gln Cys
195           260          265          270
196 Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp Ser Trp Glu

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197          275          280          285
198 Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr Gly Arg Gly
199          290          295          300
200 Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro Ser Ser Ser
201 305          310          315          320
202 Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln Pro Asn Ser
203          325          330          335
204 His Pro Ile Gln Trp Leu Asp Asp Asp Lys Ala Ala Gly Ser Ile
205          340          345          350
206 Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly Gly Ser Gly Ala Phe Pro
207          355          360          365
208 Pro Gly His Phe Lys Asp Pro Lys Arg Leu Tyr Cys Lys Asn Gly Gly
209          370          375          380
210 Phe Phe Leu Arg Ile His Pro Asp Gly Arg Val Asp Gly Val Arg Glu
211 385          390          395          400
212 Lys Ser Asp Pro His Ile Lys Leu Gln Leu Gln Ala Glu Glu Arg Gly
213          405          410          415
214 Val Val Ser Ile Lys Gly Val Cys Ala Asn Arg Tyr Leu Ala Met Lys
215          420          425          430
216 Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys Val Thr Asp Glu Cys Phe
217          435          440          445
218 Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr Asn Thr Tyr Arg Ser Arg
219          450          455          460
220 Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys Arg Thr Gly Gln Tyr Lys
221 465          470          475          480
222 Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys Ala Ile Leu Phe Leu Pro
223          485          490          495
224 Met Ser Ala Lys Ser
225          500
226 <210> SEQ ID NO: 5
227 <211> LENGTH: 400
228 <212> TYPE: PRT
229 <213> ORGANISM: Artificial Sequence
W--> 230 <220> FEATURE:
231 <223> OTHER INFORMATION: Description of Artificial Sequence:Hybrid
232 Polypeptide of Human Fibronectin Collagen-Binding
233 Domain and Human Epidermal Growth Factor
W--> 234 <220> FEATURE:
W--> 235 <221> NAME/KEY: INIT _MET
236 <222> LOCATION: (1)
W--> 237 <220> FEATURE:
238 <221> NAME/KEY: DOMAIN
239 <222> LOCATION: (2)..(341)
240 <223> OTHER INFORMATION: /note="human fibronectin collagen-binding domain"
W--> 241 <220> FEATURE:
242 <221> NAME/KEY: PEPTIDE
243 <222> LOCATION: (343)..(347)
244 <223> OTHER INFORMATION: /note=" enterokinase recognition sequence"
W--> 245 <220> FEATURE:

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VERIFICATION SUMMARY

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Input Set : A:\substitute SL 029650-103.txt

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L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:283 W: Missing Blank Line separator, <140> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application Number
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:283 W: Missing Blank Line separator, <220> field identifier
L:18 M:283 W: Missing Blank Line separator, <220> field identifier
L:19 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:283 W: Missing Blank Line separator, <220> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:31 M:283 W: Missing Blank Line separator, <400> field identifier
L:80 M:283 W: Missing Blank Line separator, <220> field identifier
L:84 M:283 W: Missing Blank Line separator, <220> field identifier
L:88 M:283 W: Missing Blank Line separator, <220> field identifier
L:92 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:283 W: Missing Blank Line separator, <220> field identifier
L:121 M:283 W: Missing Blank Line separator, <220> field identifier
L:125 M:283 W: Missing Blank Line separator, <220> field identifier
L:129 M:283 W: Missing Blank Line separator, <400> field identifier
L:142 M:283 W: Missing Blank Line separator, <220> field identifier
L:146 M:283 W: Missing Blank Line separator, <220> field identifier
L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:149 M:283 W: Missing Blank Line separator, <220> field identifier
L:153 M:283 W: Missing Blank Line separator, <220> field identifier
L:157 M:283 W: Missing Blank Line separator, <220> field identifier
L:161 M:283 W: Missing Blank Line separator, <400> field identifier
L:230 M:283 W: Missing Blank Line separator, <220> field identifier
L:234 M:283 W: Missing Blank Line separator, <220> field identifier
L:235 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:237 M:283 W: Missing Blank Line separator, <220> field identifier
L:241 M:283 W: Missing Blank Line separator, <220> field identifier
L:245 M:283 W: Missing Blank Line separator, <220> field identifier
L:249 M:283 W: Missing Blank Line separator, <400> field identifier
L:304 M:283 W: Missing Blank Line separator, <220> field identifier
L:308 M:283 W: Missing Blank Line separator, <400> field identifier
L:314 M:283 W: Missing Blank Line separator, <220> field identifier
L:318 M:283 W: Missing Blank Line separator, <220> field identifier
L:319 M:283 W: Missing Blank Line separator, <400> field identifier
L:325 M:283 W: Missing Blank Line separator, <220> field identifier
L:328 M:283 W: Missing Blank Line separator, <220> field identifier
L:331 M:283 W: Missing Blank Line separator, <220> field identifier
L:334 M:283 W: Missing Blank Line separator, <220> field identifier
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L:340 M:283 W: Missing Blank Line separator, <220> field identifier
L:343 M:283 W: Missing Blank Line separator, <400> field identifier

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Input Set : A:\substitute SL 029650-103.txt

Output Set: N:\CRF3\11162001\I934706.raw

L:366 M:283 W: Missing Blank Line separator, <220> field identifier
L:369 M:283 W: Missing Blank Line separator, <400> field identifier
L:375 M:283 W: Missing Blank Line separator, <220> field identifier
L:378 M:283 W: Missing Blank Line separator, <400> field identifier
L:384 M:283 W: Missing Blank Line separator, <220> field identifier
L:388 M:283 W: Missing Blank Line separator, <220> field identifier
L:393 M:283 W: Missing Blank Line separator, <400> field identifier